to nondetectable levels in chromoplasts. Piechulla *et al.*, *Plant Mol. Biol.* (1986) 7:367-376.

Summary of the Invention

Novel methods and DNA constructs are provided for transforming plants employing T-DNA and a Ti- or Ri-plasmid for heterologous DNA introduction and integration into the plant genome. Transformation without gall formation of plant cells which have historically not been *Agrobacterium* hosts is achieved with successful expression of the heterologous DNA. Additionally, DNA constructs are provided which are employed in manipulating plant cells to provide for regulated transcription, such as light inducible transcription, in a plant tissue or plant part of interest at particular stages of plant growth or in response to external control. Particularly, transcriptional regions from seed storage proteins, seed coat proteins or acyl carrier protein are joined to other than the homologous gene and introduced into a plant cell host for integration into the genome to provide for seed-specific transcription. The constructs provide for modulation of expression of endogenous products as well as production of exogenous products in the seed. Novel DNA constructions also are provided employing a fruit-specific promoter, particularly a promoter from a gene active beginning at or shortly after anthesis or beginning at the breaker stage, joined to a DNA sequence of interest and a transcriptional termination region. A DNA construct may be introduced into a plant cell host for integration into the genome and transcription regulated at a time at or subsequent to anthesis. In this manner, high levels of RNA and, as appropriate, polypeptides, may be achieved during formation and/or ripening of fruit.

Also of interest is a transcriptional initiation region which is activated at or shortly after anthesis, so that in the early development of the fruit, it provides the desired level of transcription of the sequence of interest. Normally, the sequence of interest will be involved in affecting the process in the early formation of the fruit or providing a property which is desirable during the growing (expansion) period of the fruit, or at or after harvesting.

The ripening stages of the tomato may be broken down into mature green, breaker, turning, pink, light red and red. Desirably, the transcriptional initiation region maintains its activity during the expansion and maturation of the green fruit, more desirably continues active through the ripening or red fruit period. Comparable periods for other fruit are referred to as stages of ripening. The invention is not limited to those transcriptional initiation regions which are activated at or shortly after anthesis but also includes transcriptional initiation regions which are activated at any of the ripening stages of the fruit. An example of a fruit-specific transcriptional initiation region is the one referred to as 2A11 which regulates the expression of a 2A11 cDNA sequence described in the Experimental section. The 2A11 transcriptional initiation region provides for an abundant messenger, being activated at or shortly after anthesis and remaining active until the red fruit stage. The expressed protein is a sulfur-rich protein similar to other plant storage proteins in sulfur content and size.

Also of interest is a transcriptional initiation region which regulates expression of the enzyme polygalacturonase, an enzyme which plays an important role in fruit softening and/or rotting. The polygalacturonase